



SEQUENCE LISTING

<110> LAMBERT, Bart
JANSENS, Stefan
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<120> New Bacillus Thuringiensis Strains and Their Insecticidal
Proteins

<130> 2428-0125P

<140> New

<141> 2003-10-20

<150> US 09/220,806

<151> 1998-12-28

<150> US 08/379,656

<151> 1995-03-23

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 19

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> misc_feature

<222> (1)..(19)

<223> This probe is a part of the coding DNA strand of the cryIG gene,
described by Smulevitch et al. (1991). This probe is used to
isolate the bTS02618A gene from its containing strain.

<400> 1

ttctgtacta ttgattgta

19

<210> 2

<211> 1561

<212> DNA

<213> Bacillus thuringiensis

<220>

<221> misc_feature

<222> (1)..(1561)

<223> Contains the translation initiation codon of the bTS02618A gene.

<220>

<221> misc_feature

<222> (708)..(708)

<223> n = a, c, g, t, any, unknown, or other.

<400> 2

aaaaagaaat aggaataaat actatccatt ttttcaagaa atattttttt attagaaagg	60
aatctttctt acacgggaaa atcctaagat tgagagtaaa gatatatata tataaataca	120
ataaagagtt tgtcaggatt tttgaaagat atgatatgaa catgcactag atttatagta	180
taggaggaaa aagtatgaat cgaaataatc aaaatgaata tgaaattatt gatgcccccc	240
attgtgggtg tccatcagat gacgatgtga ggtatccttt ggcaagtgc ccaaatgcag	300
cgttacaaaa tatgaactat aaagattact tacaaatgac agatgaggac tacactgatt	360
cttatataaa tcctagttta tctattagtgt gtagagatgc agttcagact gcgcttactg	420
ttgttgggag aatactcggg gcttttaggtg ttccgttttc tggacaaata gtgagttttt	480
atcaattcct tttaaataca ctgtggccag ttaatgatac agctatatgg gaagctttca	540
tgcgacaggt ggaggaactt gtcaatcaac aaataacaga atttgcaaga aatcaggcac	600
ttgcaagatt gcaaggatta ggagactctt ttaatgtata tcaacgttcc cttcaaaatt	660
ggttggctga tcgaaatgat acacgaaatt taagtgttgt tcgtgctnaa tttatagctt	720
tagaccttga ttttgttaat gctattccat tgtttgcagt aaatggacag caggttccat	780
tactgtcagt atatgcacaa gctgtgaatt tacatttggt attattaaaa gatgcatctc	840
tttttggaaga aggatgggga ttcacacagg gggaaatttc cacatattat gaccgtcaat	900
tggaactaac cgctaagtac actaattact gtgaaacttg gtataataca ggttttagatc	960
gtttaagagg aacaaatact gaaagttggt taagatatca tcaattccgt agagaaatga	1020
ctttagtggg attagatggt gtggcgctat ttccatatta tgatgtacga ctttatccaa	1080
cgggatcaaa cccacagctt acacgtgagg tatatacaga tccgattgta tttaatccac	1140
cagctaattgt tggactttgc cgacgttggg gtactaatcc ctataatact ttttctgagc	1200
tcgaaaatgc cttcattcgc ccaccacatc tttttgatag gctgaatagc ttaacaatca	1260
gcagtaatcg atttccagtt tcatctaatt ttatggatta ttggtcagga catacgttac	1320
gccgtagtta tctgaacgat tcagcagtac aagaagatag ttatggccta attacaacca	1380
caagagcaac aattaatccc ggagttgatg gaacaaaccg catagagtca acggcagtag	1440
attttcgttc tgcattgata ggtatatatg gcgtgaatag agcttctttt gtcccaggag	1500
gcttgtttaa tggtagcact tctcctgcta atggaggatg tagagatctc tatgatacaa	1560
a	1561

<210> 3
 <211> 1554
 <212> DNA
 <213> *Bacillus thuringiensis*

<220>
 <221> misc_feature
 <222> (1146)..(1148)
 <223> Presumed translational stop codon of bTS02618A gene.

<400> 3
 aaaattatcc aacatacatt tatcaaaaag tagatgcac ggtgttaaag cttatacac 60
 gctatagact agatggattt gtgaagagta gtcaagattt agaaattgat ctcacccacc 120
 atcataaagt ccatcttgta aaaaatgtac cagataattt agtatctgat acttactcag 180
 atggttcttg cagcggaaac aaccgttggt atgaacagca tcaggtagat atgcagctag 240
 atgaggagca tcatccaatg gattgctgtg aagcggctca aacacatgag ttttcttcct 300
 atattaatac aggggatcta aatgcaagt tagatcaggg catttggggt gtattaaaag 360
 ttcgaacaac agatgggtat gcgacgttag gaaatcttga attggttagag gttgggccat 420
 tatcgggtga atctctagaa cggaacaaa gagataatgc gaaatggaat gcagagctag 480
 gaagaaaacg tgcagaaata gatcgtgtgt atttagctgc gaaacaagca attaatcatc 540
 tgtttgtaga ctatcaagat caacaattaa atccagaaat tgggctagca gaaattaatg 600
 aagcttcaaa tcttgtagag tcaatttcgg gtgtatatag tgatacacta ttacagattc 660
 ctgggattaa ctacgaaatt tacacagagt tatccgatcg cttacaaca gcacgcatc 720
 tgtatacgtc tagaaatgcg gtgcaaatg gagacttta cagtgggtcta gatagttgga 780
 atacaactat ggatgcacg gttcagcaag atggcaatat gcatttctta gttctttcgc 840
 attgggatgc acaagtttcc caacaattga gagtaaacc gaattgtaag tatgtcttac 900
 gtgtgacagc aagaaaagta ggaggcggag atggatacgt cacaatccga gatggcgctc 960
 atcaccaaga aactcttaca tttaatgcat gtgactacga tgtaaagggt acgtatgtca 1020
 atgacaattc gtatataaca gaagaagtgg tattctaccc agagacaaaa catatgtggg 1080
 tagaggtaga tgaatccgaa gggtcattct atatagacag tattgagttt attgaaacac 1140
 aagagtagaa gagggggatc ctaacgtata gcaactatga gaggatactc cgtacaaaca 1200
 aagattaaaa aaaggtaaaa tgaatagaac cccctactgg tagaaggacc gataggggggt 1260
 tcttacatga aaaaatgtag ctgtttacta aggtgtataa aaaacagcat atctgataga 1320
 aaaaagttag taccttataa agaaagaatt ccattcacag tttcgggtatc atataaataa 1380

tgataggggt atccttctta ttacattat ttttcgcaat tatctcgacg ttcttctttc 1440
cgctcacaat gatgatgatc atgacaacaa tcgcgtccat agcgaactct ttcgatatta 1500
ataatatcta aactcgtgta gcagtcattt ccattttttt tgatccagta aata 1554

<210> 4
<211> 4344
<212> DNA
<213> *Bacillus thuringiensis*

<220>
<221> CDS
<222> (668)..(4141)
<223> Encompasses the entire sequence of SEQ ID NO:2: from nucleotide position 474 to 2034 in SEQ ID NO:4; also encompasses part of the sequence of SEQ ID NO:3: from nucleotide position 2994 to nucleotide position 4344 in SEQ ID NO:4; SEQ ID NO:3 shows additional

<220>
<223> nucleotides, located downstream (3') from the sequence shown in SEQ ID NO:4 (nucleotide position 1352 to nucleotide position 1554 in SEQ ID NO:3)

<400> 4
gaattcgagc tcggtacctt ttcagtgtat cgtttccctt ccatcagggt ttcaaattga 60
aaagccgaat gatttgaaac ttgtttacga tgtaagtcatt ttgtctatga cgaaagatac 120
gtgtaaaaaa cgtattgaga ttgatgaatg tggacaagta gaaattgact tacaagtatt 180
aaagattaag ggtgtccttt cttttatcgg aaatttctct attgaacctt ttctgtgtga 240
aaacatgtat acaacggttg atagagatcc gtctatttcc ttaagtttcc aagatacgggt 300
atatgtggac catattttta aatatagcgt ccaacaacta ccatattatg taattgatgg 360
tgatcatatt caagtacgtg atttacaat caaactgatg aaagagaatc cgcaatctgc 420
tcaagtatca ggtttgtttt gttttgtata tgagtaagaa ccgaagggtt gtaaaaaaga 480
aataggaata aatactatcc attttttcaa gaaatatttt tttattagaa aggaatcttt 540
cttacacggg aaaatcctaa gattgagagt aaagatatat atatataaat acaataaaga 600
gtttgtcagg atttttgaaa gatatgatat gaacatgcac tagatttata gtataggagg 660
aaaaagt atg aat cga aat aat caa aat gaa tat gaa att att gat gcc 709
Met Asn Arg Asn Asn Gln Asn Glu Tyr Glu Ile Ile Asp Ala
1 5 10
ccc cat tgt ggg tgt cca tca gat gac gat gtg agg tat cct ttg gca 757
Pro His Cys Gly Cys Pro Ser Asp Asp Asp Val Arg Tyr Pro Leu Ala
15 20 25 30

agt gac cca aat gca gcg tta caa aat atg aac tat aaa gat tac tta	805
Ser Asp Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu	
35 40 45	
caa atg aca gat gag gac tac act gat tct tat ata aat cct agt tta	853
Gln Met Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu	
50 55 60	
tct att agt ggt aga gat gca gtt cag act gcg ctt act gtt gtt ggg	901
Ser Ile Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly	
65 70 75	
aga ata ctc ggg gct tta ggt gtt ccg ttt tct gga caa ata gtg agt	949
Arg Ile Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser	
80 85 90	
ttt tat caa ttc ctt tta aat aca ctg tgg cca gtt aat gat aca gct	997
Phe Tyr Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala	
95 100 105 110	
ata tgg gaa gct ttc atg cga cag gtg gag gaa ctt gtc aat caa caa	1045
Ile Trp Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln	
115 120 125	
ata aca gaa ttt gca aga aat cag gca ctt gca aga ttg caa gga tta	1093
Ile Thr Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu	
130 135 140	
gga gac tct ttt aat gta tat caa cgt tcc ctt caa aat tgg ttg gct	1141
Gly Asp Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala	
145 150 155	
gat cga aat gat aca cga aat tta agt gtt gtt cgt gct caa ttt ata	1189
Asp Arg Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile	
160 165 170	
gct tta gac ctt gat ttt gtt aat gct att cca ttg ttt gca gta aat	1237
Ala Leu Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn	
175 180 185 190	
gga cag cag gtt cca tta ctg tca gta tat gca caa gct gtg aat tta	1285
Gly Gln Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu	
195 200 205	
cat ttg tta tta tta aaa gat gca tct ctt ttt gga gaa gga tgg gga	1333
His Leu Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly	
210 215 220	
ttc aca cag ggg gaa att tcc aca tat tat gac cgt caa ttg gaa cta	1381
Phe Thr Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu	
225 230 235	
acc gct aag tac act aat tac tgt gaa act tgg tat aat aca ggt tta	1429
Thr Ala Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu	
240 245 250	

gat cgt tta aga gga aca aat act gaa agt tgg tta aga tat cat caa	1477
Asp Arg Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln	
255 260 265 270	
ttc cgt aga gaa atg act tta gtg gta tta gat gtt gtg gcg cta ttt	1525
Phe Arg Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe	
275 280 285	
cca tat tat gat gta cga ctt tat cca acg gga tca aac cca cag ctt	1573
Pro Tyr Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu	
290 295 300	
aca cgt gag gta tat aca gat ccg att gta ttt aat cca cca gct aat	1621
Thr Arg Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn	
305 310 315	
gtt gga ctt tgc cga cgt tgg ggt act aat ccc tat aat act ttt tct	1669
Val Gly Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser	
320 325 330	
gag ctc gaa aat gcc ttc att cgc cca cca cat ctt ttt gat agg ctg	1717
Glu Leu Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu	
335 340 345 350	
aat agc tta aca atc agc agt aat cga ttt cca gtt tca tct aat ttt	1765
Asn Ser Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe	
355 360 365	
atg gat tat tgg tca gga cat acg tta cgc cgt agt tat ctg aac gat	1813
Met Asp Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp	
370 375 380	
tca gca gta caa gaa gat agt tat ggc cta att aca acc aca aga gca	1861
Ser Ala Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Arg Ala	
385 390 395	
aca att aat ccc gga gtt gat gga aca aac cgc ata gag tca acg gca	1909
Thr Ile Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala	
400 405 410	
gta gat ttt cgt tct gca ttg ata ggt ata tat ggc gtg aat aga gct	1957
Val Asp Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala	
415 420 425 430	
tct ttt gtc cca gga ggc ttg ttt aat ggt acg act tct cct gct aat	2005
Ser Phe Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn	
435 440 445	
gga gga tgt aga gat ctc tat gat aca aat gat gaa tta cca cca gat	2053
Gly Gly Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp	
450 455 460	
gaa agt acc gga agt tca acc cat aga cta tct cat gtt acc ttt ttt	2101
Glu Ser Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe	
465 470 475	
agc ttt caa act aat cag gct gga tct ata gct aat gca gga agt gta	2149

Ser	Phe	Gln	Thr	Asn	Gln	Ala	Gly	Ser	Ile	Ala	Asn	Ala	Gly	Ser	Val		
480						485					490						
cct	act	tat	gtt	tgg	acc	cgt	cgt	gat	gtg	gac	ctt	aat	aat	acg	att	2197	
Pro	Thr	Tyr	Val	Trp	Thr	Arg	Arg	Asp	Val	Asp	Leu	Asn	Asn	Thr	Ile		
495					500					505					510		
acc	cca	aat	aga	att	aca	caa	tta	cca	ttg	gta	aag	gca	tct	gca	cct	2245	
Thr	Pro	Asn	Arg	Ile	Thr	Gln	Leu	Pro	Leu	Val	Lys	Ala	Ser	Ala	Pro		
				515					520					525			
gtt	tcg	ggg	act	acg	gtc	tta	aaa	ggg	cca	gga	ttt	aca	gga	ggg	ggg	2293	
Val	Ser	Gly	Thr	Thr	Val	Leu	Lys	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Gly		
			530					535					540				
ata	ctc	cga	aga	aca	act	aat	ggc	aca	ttt	gga	acg	tta	aga	gta	acg	2341	
Ile	Leu	Arg	Arg	Thr	Thr	Asn	Gly	Thr	Phe	Gly	Thr	Leu	Arg	Val	Thr		
			545				550					555					
gtt	aat	tca	cca	tta	aca	caa	caa	tat	cgc	cta	aga	gtt	cgt	ttt	gcc	2389	
Val	Asn	Ser	Pro	Leu	Thr	Gln	Gln	Tyr	Arg	Leu	Arg	Val	Arg	Phe	Ala		
	560					565					570						
tca	aca	gga	aat	ttc	agt	ata	agg	gta	ctc	cgt	gga	ggg	gtt	tct	atc	2437	
Ser	Thr	Gly	Asn	Phe	Ser	Ile	Arg	Val	Leu	Arg	Gly	Gly	Val	Ser	Ile		
575					580					585					590		
ggg	gat	gtt	aga	tta	ggg	agc	aca	atg	aac	aga	ggg	cag	gaa	cta	act	2485	
Gly	Asp	Val	Arg	Leu	Gly	Ser	Thr	Met	Asn	Arg	Gly	Gln	Glu	Leu	Thr		
				595					600					605			
tac	gaa	tcc	ttt	ttc	aca	aga	gag	ttt	act	act	act	ggg	ccg	ttc	aat	2533	
Tyr	Glu	Ser	Phe	Phe	Thr	Arg	Glu	Phe	Thr	Thr	Thr	Gly	Pro	Phe	Asn		
			610					615					620				
ccg	cct	ttt	aca	ttt	aca	caa	gct	caa	gag	att	cta	aca	gtg	aat	gca	2581	
Pro	Pro	Phe	Thr	Phe	Thr	Gln	Ala	Gln	Glu	Ile	Leu	Thr	Val	Asn	Ala		
		625					630					635					
gaa	ggg	gtt	agc	acc	ggg	ggg	gaa	tat	tat	ata	gat	aga	att	gaa	att	2629	
Glu	Gly	Val	Ser	Thr	Gly	Gly	Glu	Tyr	Tyr	Ile	Asp	Arg	Ile	Glu	Ile		
	640					645					650						
gtc	cct	gtg	aat	ccg	gca	cga	gaa	gcg	gaa	gag	gat	tta	gaa	gcg	gcg	2677	
Val	Pro	Val	Asn	Pro	Ala	Arg	Glu	Ala	Glu	Glu	Asp	Leu	Glu	Ala	Ala		
655					660					665					670		
aag	aaa	gcg	gtg	gcg	agc	ttg	ttt	aca	cgt	aca	agg	gac	gga	tta	cag	2725	
Lys	Lys	Ala	Val	Ala	Ser	Leu	Phe	Thr	Arg	Thr	Arg	Asp	Gly	Leu	Gln		
				675					680					685			
gta	aat	gtg	aca	gat	tat	caa	gtg	gac	caa	gcg	gca	aat	tta	gtg	tca	2773	
Val	Asn	Val	Thr	Asp	Tyr	Gln	Val	Asp	Gln	Ala	Ala	Asn	Leu	Val	Ser		
			690					695					700				
tgc	tta	tcc	gat	gaa	caa	tat	ggg	cat	gac	aaa	aag	atg	tta	ttg	gaa	2821	
Cys	Leu	Ser	Asp	Glu	Gln	Tyr	Gly	His	Asp	Lys	Lys	Met	Leu	Leu	Glu		

705	710	715	
gcg gta aga gcg gca aaa cgc ctc agc cgc gaa cgc aac tta ctt caa Ala Val Arg Ala Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln 720 725 730			2869
gat cca gat ttt aat aca atc aat agt aca gaa gag aat ggc tgg aag Asp Pro Asp Phe Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys 735 740 745 750			2917
gca agt aac ggt gtt act att agc gag ggc ggt cca ttc ttt aaa ggt Ala Ser Asn Gly Val Thr Ile Ser Glu Gly Gly Pro Phe Phe Lys Gly 755 760 765			2965
cgt gca ctt cag tta gca agc gca aga gaa aat tat cca aca tac att Arg Ala Leu Gln Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile 770 775 780			3013
tat caa aaa gta gat gca tcg gtg tta aag cct tat aca cgc tat aga Tyr Gln Lys Val Asp Ala Ser Val Leu Lys Pro Tyr Thr Arg Tyr Arg 785 790 795			3061
cta gat gga ttt gtg aag agt agt caa gat tta gaa att gat ctc atc Leu Asp Gly Phe Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile 800 805 810			3109
cac cat cat aaa gtc cat ctt gta aaa aat gta cca gat aat tta gta His His His Lys Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val 815 820 825 830			3157
tct gat act tac tca gat ggt tct tgc agc gga atc aac cgt tgt gat Ser Asp Thr Tyr Ser Asp Gly Ser Cys Ser Gly Ile Asn Arg Cys Asp 835 840 845			3205
gaa cag cat cag gta gat atg cag cta gat gcg gag cat cat cca atg Glu Gln His Gln Val Asp Met Gln Leu Asp Ala Glu His His Pro Met 850 855 860			3253
gat tgc tgt gaa gcg gct caa aca cat gag ttt tct tcc tat att aat Asp Cys Cys Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asn 865 870 875			3301
aca ggg gat cta aat gca agt gta gat cag ggc att tgg gtt gta tta Thr Gly Asp Leu Asn Ala Ser Val Asp Gln Gly Ile Trp Val Val Leu 880 885 890			3349
aaa gtt cga aca aca gat ggg tat gcg acg tta gga aat ctt gaa ttg Lys Val Arg Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu 895 900 905 910			3397
gta gag gtt ggg cca tta tcg ggt gaa tct cta gaa cgg gaa caa aga Val Glu Val Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg 915 920 925			3445
gat aat gcg aaa tgg aat gca gag cta gga aga aaa cgt gca gaa ata Asp Asn Ala Lys Trp Asn Ala Glu Leu Gly Arg Lys Arg Ala Glu Ile 930 935 940			3493

gat cgt gtg tat tta gct gcg aaa caa gca att aat cat ctg ttt gta	3541
Asp Arg Val Tyr Leu Ala Ala Lys Gln Ala Ile Asn His Leu Phe Val	
945 950 955	
gac tat caa gat caa caa tta aat cca gaa att ggg cta gca gaa att	3589
Asp Tyr Gln Asp Gln Gln Leu Asn Pro Glu Ile Gly Leu Ala Glu Ile	
960 965 970	
aat gaa gct tca aat ctt gta gag tca att tcg ggt gta tat agt gat	3637
Asn Glu Ala Ser Asn Leu Val Glu Ser Ile Ser Gly Val Tyr Ser Asp	
975 980 985 990	
aca cta tta cag att cct ggg att aac tac gaa att tac aca gag tta	3685
Thr Leu Leu Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu	
995 1000 1005	
tcc gat cgc tta caa caa gca tcg tat ctg tat acg tct aga aat	3730
Ser Asp Arg Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn	
1010 1015 1020	
gcg gtg caa aat gga gac ttt aac agt ggt cta gat agt tgg aat	3775
Ala Val Gln Asn Gly Asp Phe Asn Ser Gly Leu Asp Ser Trp Asn	
1025 1030 1035	
aca act atg gat gca tcg gtt cag caa gat ggc aat atg cat ttc	3820
Thr Thr Met Asp Ala Ser Val Gln Gln Asp Gly Asn Met His Phe	
1040 1045 1050	
tta gtt ctt tcg cat tgg gat gca caa gtt tcc caa caa ttg aga	3865
Leu Val Leu Ser His Trp Asp Ala Gln Val Ser Gln Gln Leu Arg	
1055 1060 1065	
gta aat ccg aat tgt aag tat gtc tta cgt gtg aca gca aga aaa	3910
Val Asn Pro Asn Cys Lys Tyr Val Leu Arg Val Thr Ala Arg Lys	
1070 1075 1080	
gta gga ggc gga gat gga tac gtc aca atc cga gat ggc gct cat	3955
Val Gly Gly Gly Asp Gly Tyr Val Thr Ile Arg Asp Gly Ala His	
1085 1090 1095	
cac caa gaa act ctt aca ttt aat gca tgt gac tac gat gta aat	4000
His Gln Glu Thr Leu Thr Phe Asn Ala Cys Asp Tyr Asp Val Asn	
1100 1105 1110	
ggg acg tat gtc aat gac aat tcg tat ata aca gaa gaa gtg gta	4045
Gly Thr Tyr Val Asn Asp Asn Ser Tyr Ile Thr Glu Glu Val Val	
1115 1120 1125	
ttc tac cca gag aca aaa cat atg tgg gta gag gtg agt gaa tcc	4090
Phe Tyr Pro Glu Thr Lys His Met Trp Val Glu Val Ser Glu Ser	
1130 1135 1140	
gaa ggt tca ttc tat ata gac agt att gag ttt att gaa aca caa	4135
Glu Gly Ser Phe Tyr Ile Asp Ser Ile Glu Phe Ile Glu Thr Gln	
1145 1150 1155	

gag tag aagaggggga tcctaacgta tagcaactat gagaggatac tccgtacaaa 4191
Glu

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<211> 1157

<212> PRT

<213> *Bacillus thuringiensis*

<400> 5

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Pro Asn Ala Ala Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Gln Met
35 40 45

Thr Asp Glu Asp Tyr Thr Asp Ser Tyr Ile Asn Pro Ser Leu Ser Ile
50 55 60

Ser Gly Arg Asp Ala Val Gln Thr Ala Leu Thr Val Val Gly Arg Ile
65 70 75 80

Leu Gly Ala Leu Gly Val Pro Phe Ser Gly Gln Ile Val Ser Phe Tyr
85 90 95

Gln Phe Leu Leu Asn Thr Leu Trp Pro Val Asn Asp Thr Ala Ile Trp
100 105 110

Glu Ala Phe Met Arg Gln Val Glu Glu Leu Val Asn Gln Gln Ile Thr
115 120 125

Glu Phe Ala Arg Asn Gln Ala Leu Ala Arg Leu Gln Gly Leu Gly Asp
130 135 140

Ser Phe Asn Val Tyr Gln Arg Ser Leu Gln Asn Trp Leu Ala Asp Arg
145 150 155 160

Asn Asp Thr Arg Asn Leu Ser Val Val Arg Ala Gln Phe Ile Ala Leu
 165 170 175

Asp Leu Asp Phe Val Asn Ala Ile Pro Leu Phe Ala Val Asn Gly Gln
 180 185 190

Gln Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Val Asn Leu His Leu
 195 200 205

Leu Leu Leu Lys Asp Ala Ser Leu Phe Gly Glu Gly Trp Gly Phe Thr
 210 215 220

Gln Gly Glu Ile Ser Thr Tyr Tyr Asp Arg Gln Leu Glu Leu Thr Ala
 225 230 235 240

Lys Tyr Thr Asn Tyr Cys Glu Thr Trp Tyr Asn Thr Gly Leu Asp Arg
 245 250 255

Leu Arg Gly Thr Asn Thr Glu Ser Trp Leu Arg Tyr His Gln Phe Arg
 260 265 270

Arg Glu Met Thr Leu Val Val Leu Asp Val Val Ala Leu Phe Pro Tyr
 275 280 285

Tyr Asp Val Arg Leu Tyr Pro Thr Gly Ser Asn Pro Gln Leu Thr Arg
 290 295 300

Glu Val Tyr Thr Asp Pro Ile Val Phe Asn Pro Pro Ala Asn Val Gly
 305 310 315 320

Leu Cys Arg Arg Trp Gly Thr Asn Pro Tyr Asn Thr Phe Ser Glu Leu
 325 330 335

Glu Asn Ala Phe Ile Arg Pro Pro His Leu Phe Asp Arg Leu Asn Ser
 340 345 350

Leu Thr Ile Ser Ser Asn Arg Phe Pro Val Ser Ser Asn Phe Met Asp
 355 360 365

Tyr Trp Ser Gly His Thr Leu Arg Arg Ser Tyr Leu Asn Asp Ser Ala
 370 375 380

Val Gln Glu Asp Ser Tyr Gly Leu Ile Thr Thr Thr Arg Ala Thr Ile
 385 390 395 400

Asn Pro Gly Val Asp Gly Thr Asn Arg Ile Glu Ser Thr Ala Val Asp
 405 410 415

Phe Arg Ser Ala Leu Ile Gly Ile Tyr Gly Val Asn Arg Ala Ser Phe
 420 425 430

Val Pro Gly Gly Leu Phe Asn Gly Thr Thr Ser Pro Ala Asn Gly Gly
 435 440 445

Cys Arg Asp Leu Tyr Asp Thr Asn Asp Glu Leu Pro Pro Asp Glu Ser
 450 455 460

Thr Gly Ser Ser Thr His Arg Leu Ser His Val Thr Phe Phe Ser Phe
 465 470 475 480

Gln Thr Asn Gln Ala Gly Ser Ile Ala Asn Ala Gly Ser Val Pro Thr
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Tyr Val Trp Thr Arg Arg Asp Val Asp Leu Asn Asn Thr Ile Thr Pro
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Asn Arg Ile Thr Gln Leu Pro Leu Val Lys Ala Ser Ala Pro Val Ser
 515 520 525

Gly Thr Thr Val Leu Lys Gly Pro Gly Phe Thr Gly Gly Gly Ile Leu
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Arg Arg Thr Thr Asn Gly Thr Phe Gly Thr Leu Arg Val Thr Val Asn
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Ser Pro Leu Thr Gln Gln Tyr Arg Leu Arg Val Arg Phe Ala Ser Thr
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Gly Asn Phe Ser Ile Arg Val Leu Arg Gly Gly Val Ser Ile Gly Asp
 580 585 590

Val Arg Leu Gly Ser Thr Met Asn Arg Gly Gln Glu Leu Thr Tyr Glu
 595 600 605

Ser Phe Phe Thr Arg Glu Phe Thr Thr Thr Gly Pro Phe Asn Pro Pro

610		615		620	
Phe Thr Phe Thr Gln Ala Gln Glu Ile Leu Thr Val Asn Ala Glu Gly					
625		630		635	640
Val Ser Thr Gly Gly Glu Tyr Tyr Ile Asp Arg Ile Glu Ile Val Pro					
		645		650	655
Val Asn Pro Ala Arg Glu Ala Glu Glu Asp Leu Glu Ala Ala Lys Lys					
		660		665	670
Ala Val Ala Ser Leu Phe Thr Arg Thr Arg Asp Gly Leu Gln Val Asn					
		675		680	685
Val Thr Asp Tyr Gln Val Asp Gln Ala Ala Asn Leu Val Ser Cys Leu					
		690		695	700
Ser Asp Glu Gln Tyr Gly His Asp Lys Lys Met Leu Leu Glu Ala Val					
705		710		715	720
Arg Ala Ala Lys Arg Leu Ser Arg Glu Arg Asn Leu Leu Gln Asp Pro					
		725		730	735
Asp Phe Asn Thr Ile Asn Ser Thr Glu Glu Asn Gly Trp Lys Ala Ser					
		740		745	750
Asn Gly Val Thr Ile Ser Glu Gly Gly Pro Phe Phe Lys Gly Arg Ala					
		755		760	765
Leu Gln Leu Ala Ser Ala Arg Glu Asn Tyr Pro Thr Tyr Ile Tyr Gln					
		770		775	780
Lys Val Asp Ala Ser Val Leu Lys Pro Tyr Thr Arg Tyr Arg Leu Asp					
785		790		795	800
Gly Phe Val Lys Ser Ser Gln Asp Leu Glu Ile Asp Leu Ile His His					
		805		810	815
His Lys Val His Leu Val Lys Asn Val Pro Asp Asn Leu Val Ser Asp					
		820		825	830
Thr Tyr Ser Asp Gly Ser Cys Ser Gly Ile Asn Arg Cys Asp Glu Gln					
		835		840	845

His Gln Val Asp Met Gln Leu Asp Ala Glu His His Pro Met Asp Cys
850 855 860

Cys Glu Ala Ala Gln Thr His Glu Phe Ser Ser Tyr Ile Asn Thr Gly
865 870 875 880

Asp Leu Asn Ala Ser Val Asp Gln Gly Ile Trp Val Val Leu Lys Val
885 890 895

Arg Thr Thr Asp Gly Tyr Ala Thr Leu Gly Asn Leu Glu Leu Val Glu
900 905 910

Val Gly Pro Leu Ser Gly Glu Ser Leu Glu Arg Glu Gln Arg Asp Asn
915 920 925

Ala Lys Trp Asn Ala Glu Leu Gly Arg Lys Arg Ala Glu Ile Asp Arg
930 935 940

Val Tyr Leu Ala Ala Lys Gln Ala Ile Asn His Leu Phe Val Asp Tyr
945 950 955 960

Gln Asp Gln Gln Leu Asn Pro Glu Ile Gly Leu Ala Glu Ile Asn Glu
965 970 975

Ala Ser Asn Leu Val Glu Ser Ile Ser Gly Val Tyr Ser Asp Thr Leu
980 985 990

Leu Gln Ile Pro Gly Ile Asn Tyr Glu Ile Tyr Thr Glu Leu Ser Asp
995 1000 1005

Arg Leu Gln Gln Ala Ser Tyr Leu Tyr Thr Ser Arg Asn Ala Val
1010 1015 1020

Gln Asn Gly Asp Phe Asn Ser Gly Leu Asp Ser Trp Asn Thr Thr
1025 1030 1035

Met Asp Ala Ser Val Gln Gln Asp Gly Asn Met His Phe Leu Val
1040 1045 1050

Leu Ser His Trp Asp Ala Gln Val Ser Gln Gln Leu Arg Val Asn
1055 1060 1065

Pro Asn Cys Lys Tyr Val Leu Arg Val Thr Ala Arg Lys Val Gly
 1070 1075 1080

Gly Gly Asp Gly Tyr Val Thr Ile Arg Asp Gly Ala His His Gln
 1085 1090 1095

Glu Thr Leu Thr Phe Asn Ala Cys Asp Tyr Asp Val Asn Gly Thr
 1100 1105 1110

Tyr Val Asn Asp Asn Ser Tyr Ile Thr Glu Glu Val Val Phe Tyr
 1115 1120 1125

Pro Glu Thr Lys His Met Trp Val Glu Val Ser Glu Ser Glu Gly
 1130 1135 1140

Ser Phe Tyr Ile Asp Ser Ile Glu Phe Ile Glu Thr Gln Glu
 1145 1150 1155